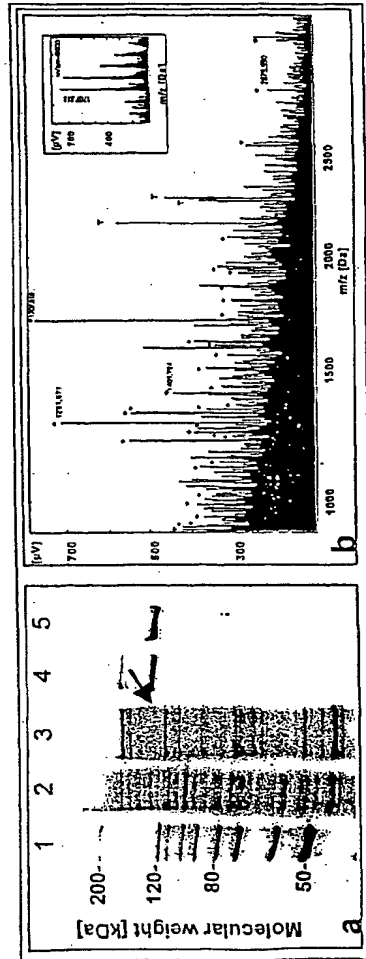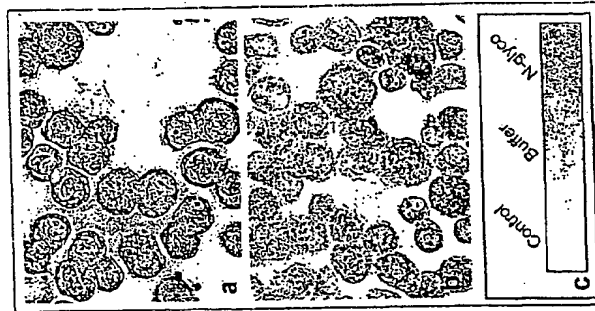Fig. 1
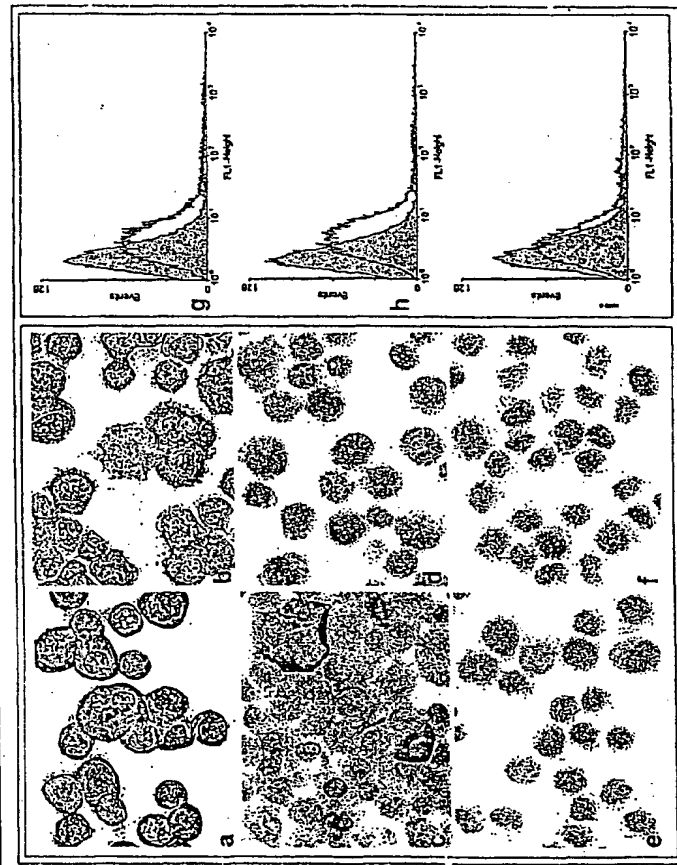
Fig. 2

Fig. 3

Fig. 4

Fig. 5

Fig. 6

Fig. 7

```
tcc tgc aag gct tct ggc tac acc ttc act gac tac tat ata aac    45
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn
 1               5                   10                  15

tgg gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag    90
Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu
                20                  25                  30

att tat cct gga agt ggt aat act tac tac aat gag aag ttc aag   135
Ile Tyr Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys
                    35                  40                  45

ggc aag gcc aca ctg act gca gac aaa tcc tcc agc aca gcc tac   180
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
                    50                  55                  60

atg cag ctc agc agc ctg aca tct gag gac tct gca gtc tat ttc   225
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
                    65                  70                  75

tgt gca aga tcg gga tta cga ccc tat gct atg gac tac tgg ggt   270
Cys Ala Arg Ser Gly Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly
                    80                  85                  90

caa gga acc tca gtc acc
Gln Gly Thr Ser Val Thr
                95
```

Fig. 8A

Fig. 8B

Nucleotide sequence of the variable region of the heavy chain (VH) of antibody NM58-49/69

CDR1

```
tcc tgc aag gct tct ggc tac acc ttc act gac tac tat ata aac
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn
 1               5                  10                 15
```
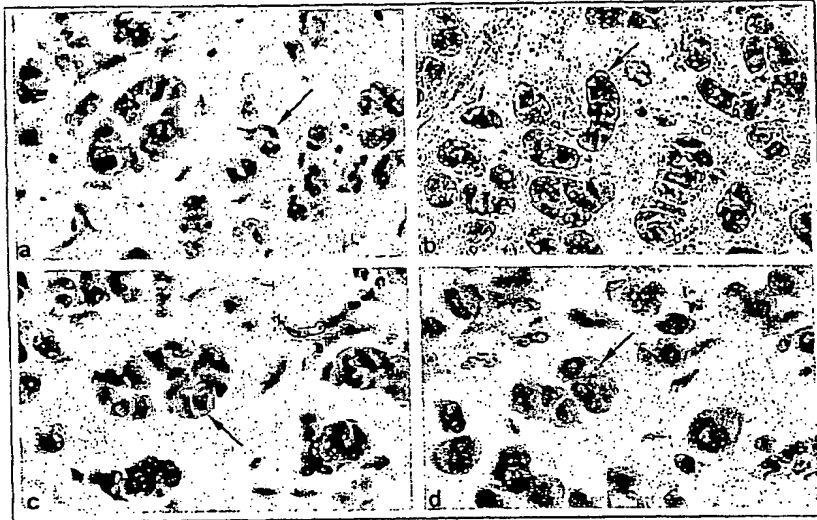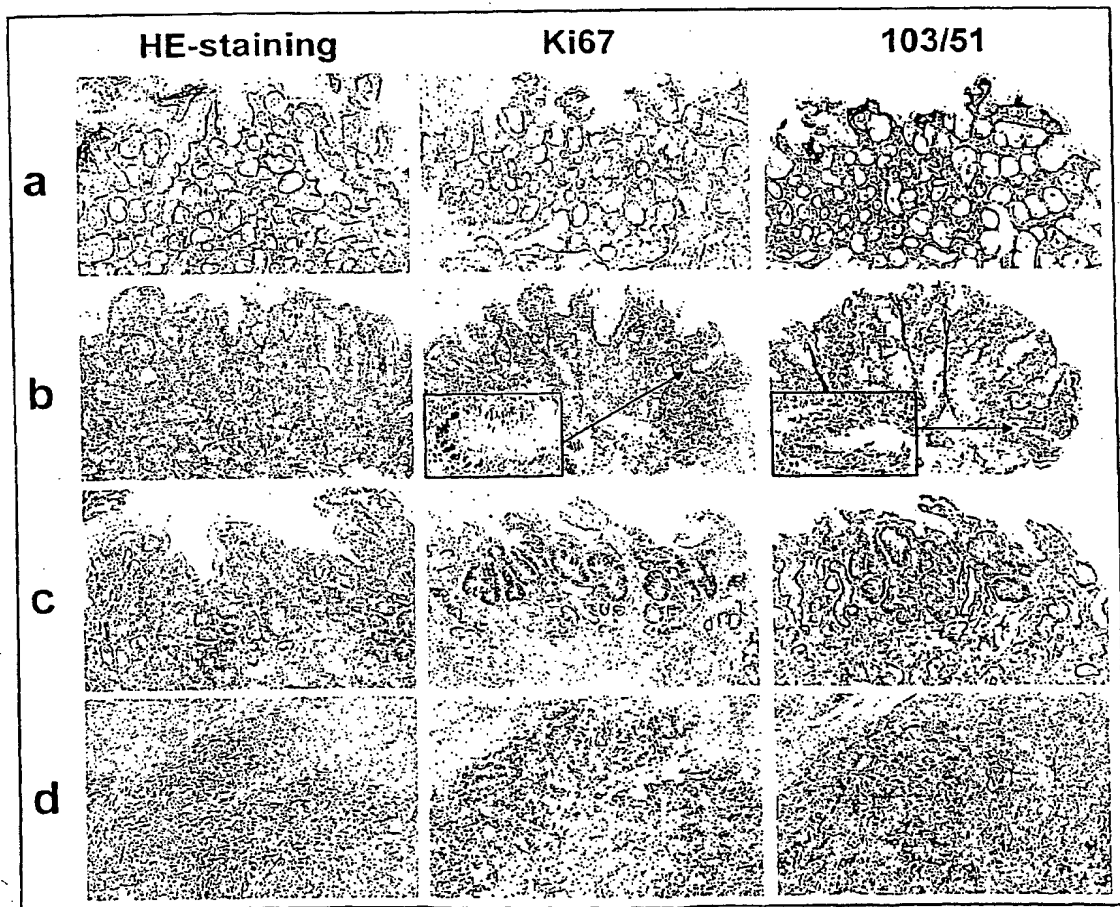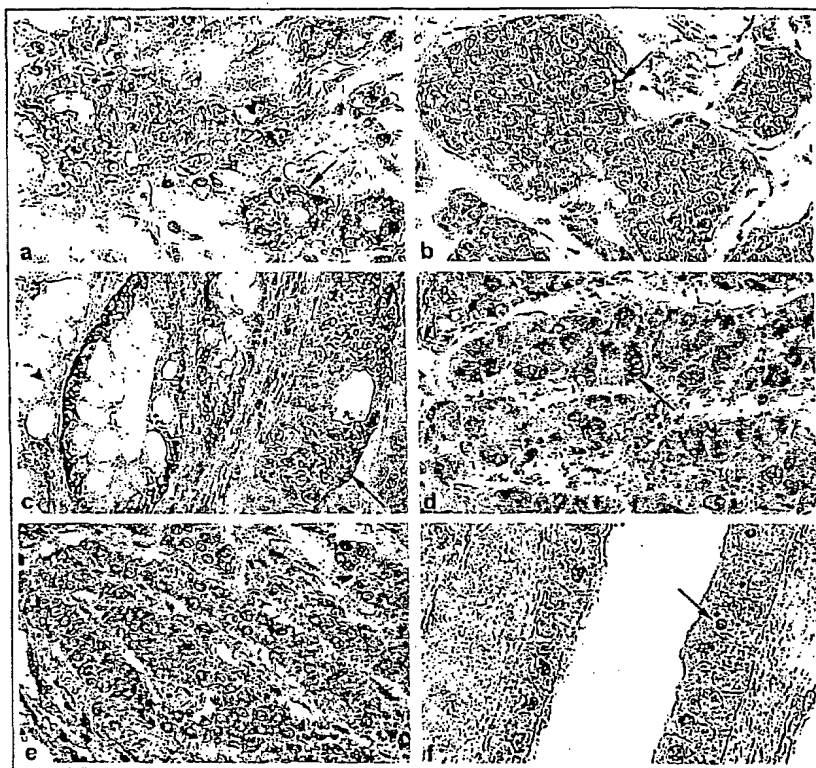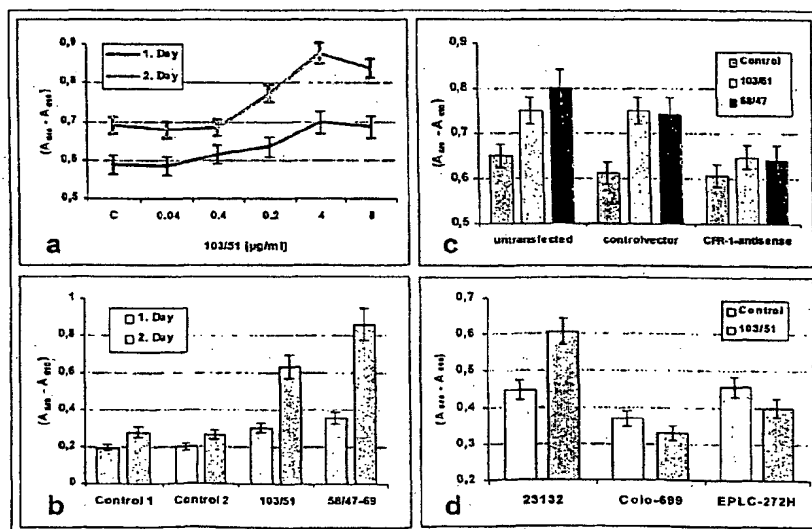
```
tgg gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag gag    90
Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Glu
              20                 25                 30
```

CDR2

```
att tat cct gga agt ggt aat act tac tac aat gag aag ttc aag    135
Ile Tyr Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys
              35                 40                 45
```

```
ggc aag gcc aca ctg act gca gac aaa tcc tcc agc aca gcc tac    180
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
              50                 55                 60
```

```
atg cag ctc agc agc ctg aca tct gag gac tct gca gtc tat ttc    225
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
              65                 70                 75
```

D-gene   CDR3   J-gene

```
tgt gca aga tcg gga tta cga ccc tat gct atg gac tac tgg ggt    270
Cys Ala Arg Ser Gly Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly
              80                 85                 90
```

```
caa gga acc tca gtc acc
Gln Gly Thr Ser Val Thr
                95
```

```
cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct    45
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
 1               5                  10                  15

tgc aga tct agt cag agc att gta cat agt aat gga aac acc tat    90
Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr
                20                  25                  30

tta gaa tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg    135
Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu
                35                  40                  45

atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc    180
Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
                50                  55                  60

agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga    225
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
                65                  70                  75

gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt tca    270
Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser
                80                  85                  90

cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa    315
His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                95                  100                 105
```

Fig. 9A

Fig. 9B

Nucleotide sequence of the variable region of the light chain (VL) of antibody NM58-49/69

```
cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct  45
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
 1               5                10                15

tgc aga tct agt cag agc att gta cat agt aat gga aac acc tat  90
Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr
            20                25                30
                        CDR1

tta gaa tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg  135
Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu
        35                40                45

atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc  180
Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
        50                55                60
            CDR2

agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga  225
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
        65                70                75

gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt tca  270
Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser
        80                85                90
                                    CDR3

cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa  315
His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
        95                100               105
```

```
gat gtg agg gag cct gaa aat gaa att tct tca gac tgc aat cat        45
Asp Val Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His
            5               10              15

ttg ttg tgg aat tat aag ctg aac cta act aca gat ccc aaa ttt        90
Leu Leu Trp Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe
            20              25              30

gaa tct gtg gcc aga gag gtt tgc aaa tct act ata aca gag att       135
Glu Ser Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile
            35              40              45

gaa gaa tgt gct gat gaa ccg gtt gga aaa ggt tac atg gtt tcc       180
Glu Glu Cys Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser
            50              55              60

tgc ttg gtg gat cac cga ggc aac atc act gag tat cag tgt cac       225
Cys Leu Val Asp His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His
            65              70              75

cag tac att acc aag atg acg gcc atc att ttt act gat tac cgt       270
Gln Tyr Ile Thr Lys Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg
            80              85              90

tta atc tgt ggc ttc atg gat gac tgc aaa aat gac atc aac att       315
Leu Ile Cys Gly Phe Met Asp Asp Cys Lys Asn Asp Ile Asn Ile
            95              100             105

ctg aaa tgt ggc agt att cgg ctt gga gaa aag gat gca cat tca       360
Leu Lys Cys Gly Ser Ile Arg Leu Gly Glu Lys Asp Ala His Ser
            110             115             120

caa ggt gag gtg gta tca tgc ttg gag aaa ggc ctg gtg aaa gaa       405
Gln Gly Glu Val Val Ser Cys Leu Glu Lys Gly Leu Val Lys Glu
            125             130             135

gca gaa gaa aga gaa ccc aag att caa gtt tct gaa ctc tgc aag       450
Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser Glu Leu Cys Lys
            140             145             150

aaa gcc att ctc cgg gtg gct gag ctg tca tcg gat gac ttt cac       495
Lys Ala Ile Leu Arg Val Ala Glu Leu Ser Ser Asp Asp Phe His
            155             160             165

tta gac cgg cat tta tat ttt gct tgc cga gat gat cgg gag cgt       540
Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp Asp Arg Glu Arg
            170             175             180

ttt tgt gaa aat aca caa gct ggt gag ggc aga gtg tat aag tgc       585
Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val Tyr Lys Cys
            185             190             195

ctc ttt aac cat aaa ttt gaa gaa tcc atg agt gaa aag tgt cga       630
Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys Cys Arg
            200             205             210
```

Fig. 10-1

```
gaa gca ctt aca acc cgc caa aag ctg att gcc cag gat tat aaa        675
Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr Lys
            215             220             225

gtc agt tat tca ttg gcc aaa tcc tgt aaa agt gac ttg aag aaa        720
Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys
            230             235             240

tac cgg tgc aat gtg gaa aac ctt ccg cga tcg cgt gaa gcc agg        765
Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg
            245             250             255

ctc tcc tac ttg tta atg tgc ctg gag tca gct gta cac aga ggg        810
Leu Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly
            260             265             270

cga caa gtc agc agt gag tgc cag ggg gag atg ctg gat tac cga        855
Arg Gln Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg
            275             280             285

cgc atg ttg atg gaa gac ttt tct ctg agc cct gag atc atc cta        900
Arg Met Leu Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu
            290             295             300

agc tgt cgg ggg gag att gaa cac cat tgt tcc gga tta cat cga        945
Ser Cys Arg Gly Glu Ile Glu His His Cys Ser Gly Leu His Arg
            305             310             315

aaa ggg cgg acc cta cac tgt ctg atg aaa gta gtt cga ggg gag        990
Lys Gly Arg Thr Leu His Cys Leu Met Lys Val Val Arg Gly Glu
            320             325             330

aag ggg aac ctt gga atg aac tgc cag cag gcg ctt caa aca ctg        1035
Lys Gly Asn Leu Gly Met Asn Cys Gln Gln Ala Leu Gln Thr Leu
            335             340             345

att cag gag act gac cct ggt gca gat tac cgc att gat cga gct        1080
Ile Gln Glu Thr Asp Pro Gly Ala Asp Tyr Arg Ile Asp Arg Ala
            350             355             360

ttg aat gaa gct tgt gaa tct gta atc cag aca gcc tgc aaa cat        1125
Leu Asn Glu Ala Cys Glu Ser Val Ile Gln Thr Ala Cys Lys His
            365             370             375

ata aga tct gga gac cca atg atc ttg tcg tgc ctg atg gaa cat        1170
Ile Arg Ser Gly Asp Pro Met Ile Leu Ser Cys Leu Met Glu His
            380             385             390

tta tac aca gag aag atg gta gaa gac tgt gaa cac cgt ctc tta        1215
Leu Tyr Thr Glu Lys Met Val Glu Asp Cys Glu His Arg Leu Leu
            395             400             405

gag ctg cag tat ttc atc tcc cgg gat tgg aag ctg gac cct gtc        1260
Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys Leu Asp Pro Val
            410             415             420

ctg tac cgc aag tgc cag gga gac gct tct cgt ctt tgc cac acc        1305
Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu Cys His Thr
            425             430             435

cac ggt tgg aat gag acc agc gaa ttt atg cct cag gga gct gtg        1350
His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly Ala Val
            440             445             450

ttc tct tgt tta tac aga cac gcc tac cgc act gag gaa cag gga        1395
Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln Gly
            455             460             465
```

Fig. 10-2

```
agg agg ctc tca cgg gag tgc cga gct gaa gtc caa agg atc cta          1440
Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu
            470             475                 480

cac cag cgt gcc atg gat gtc aag ctg gat cct gcc ctc cag gat          1485
His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp
            485             490                 495

aag tgc ctg att gat ctg gga aaa tgg tgc agt gag aaa aca gag          1530
Lys Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu
            500             505                 510

act gga cag aag ctg gag tgc ctt cag gac cat ctg gat gac tta          1575
Thr Gly Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu
            515             520                 525

gtg gtg gag tgt aga gat ata gtt ggc aac ctc act gag tta gaa          1620
Val Val Glu Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu
            530             535                 540

tca gag gat att caa ata gaa gcc ttg ctg atg aga gcc tgt gag          1665
Ser Glu Asp Ile Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu
            545             550                 555

ccc ata att cag aac ttc tgc cac gat gtg gca gat aac cag ata          1710
Pro Ile Ile Gln Asn Phe Cys His Asp Val Ala Asp Asn Gln Ile
            560             565                 570

gac tcc ggg gac ctg atg gag tgt ctg ata cag aac aaa cac cag          1755
Asp Ser Gly Asp Leu Met Glu Cys Leu Ile Gln Asn Lys His Gln
            575             580                 585

aag gac atg aac gag aag tgt gcc atc gga gtt acc cac ttc cag          1800
Lys Asp Met Asn Glu Lys Cys Ala Ile Gly Val Thr His Phe Gln
            590             595                 600

ctg gtg cag atg aag gat ttt cgg ttt tct tac aag ttt aaa atg          1845
Leu Val Gln Met Lys Asp Phe Arg Phe Ser Tyr Lys Phe Lys Met
            605             610                 615

gcc tgc aag gag gac gtg ttg aag ctt tgc cca aac ata aaa aag          1890
Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro Asn Ile Lys Lys
            620             625                 630

aag gtg gac gtg gtg atc tgc ctg agc acg acc gtg cgc aat gac          1935
Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val Arg Asn Asp
            635             640                 645

act ctg cag gaa gcc aag gag cac agg gtg tcc ctg aag tgc cgc          1980
Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys Cys Arg
            650             655                 660

agg cag ctc cgt gtg gag gag ctg gag atg acg gag gac atc cgc          2025
Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile Arg
            665             670                 675

ttg gag cca gat cta tac gaa gcc tgc aag agt gac atc aaa aac          2070
Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn
            680             685                 690

ttc tgt tcc gct gtg caa tat ggc aac gct cag att atc gaa tgt          2115
Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys
            695             700                 705

ctg aaa gaa aac aag aag cag cta agc acc cgc tgc cac caa aaa          2160
Leu Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys
            710             715                 720
```

Fig. 10-3

```
gta ttt aag ctg cag gag aca gag atg atg gac cca gag cta gac          2205
Val Phe Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp
            725                 730                 735

tac acc ctc atg agg gtc tgc aag cag atg ata aag aag ttc tgt          2250
Tyr Thr Leu Met Arg Val Cys Lys Gln Met Ile Lys Lys Phe Cys
            740                 745                 750

ccg gaa gca gat tct aaa acc atg ttg cag tgc ttg aag caa aat          2295
Pro Glu Ala Asp Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn
            755                 760                 765

aaa aac agt gaa ttg atg gat ccc aaa tgc aaa cag atg ata acc          2340
Lys Asn Ser Glu Leu Met Asp Pro Lys Cys Lys Gln Met Ile Thr
            770                 775                 780

aag cgc cag atc acc cag aac aca gat tac cgc tta aac ccc atg          2385
Lys Arg Gln Ile Thr Gln Asn Thr Asp Tyr Arg Leu Asn Pro Met
            785                 790                 795

tta aga aaa gcc tgt aaa gct gac att cct aaa ttc tgt cac ggt          2430
Leu Arg Lys Ala Cys Lys Ala Asp Ile Pro Lys Phe Cys His Gly
            800                 805                 810

atc ctg act aag gcc aag gat gat tca gaa tta gaa gga caa gtc          2475
Ile Leu Thr Lys Ala Lys Asp Asp Ser Glu Leu Glu Gly Gln Val
            815                 820                 825

atc tct tgc ctg aag ctg aga tat gct gac cag cgc ctg tct tca          2520
Ile Ser Cys Leu Lys Leu Arg Tyr Ala Asp Gln Arg Leu Ser Ser
            830                 835                 840

gac tgt gaa gac cag atc cga atc att atc cag gag tcc gcc ctg          2565
Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile Gln Glu Ser Ala Leu
            845                 850                 855

gac tac cgc ctg gat cct cag ctc cag ctg cac tgc tca gac gag          2610
Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His Cys Ser Asp Glu
            860                 865                 870

atc tcc agt cta tgt gct gaa gaa gca gca gcc caa gag cag aca          2655
Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Ala Gln Glu Gln Thr
            875                 880                 885

ggt cag gtg gag gag tgc ctc aag gtc aac ctg ctc aag atc aaa          2700
Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys Ile Lys
            890                 895                 900

aca gaa ttg tgt aaa aag gaa gtg cta aac atg ctg aag gaa agc          2745
Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu Ser
            905                 910                 915

aaa gca gac atc ttt gtt gac ccg gta ctt cat act gct tgt gcc          2790
Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala
            920                 925                 930

ctg gac att aaa cac cac tgc gca gcc atc acc cct ggc cgc ggg          2835
Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg Gly
            935                 940                 945

cgt caa atg tcc tgt ctc atg gaa gca ctg gag gat aag cgg gtg          2880
Arg Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val
            950                 955                 960

agg tta cag ccc gag tgc aaa aag cgc ctc aat gac cgg att gag          2925
Arg Leu Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu
            965                 970                 975
```

Fig. 10-4

```
atg tgg agt tac gca gca aag gtg gcc cca gca gat ggc ttc tct          2970
Met Trp Ser Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser
                980             985                 990

gat ctt gcc atg caa gta atg acg tct cca tct aag aac tac att          3015
Asp Leu Ala Met Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile
                995             1000                1005

ctc tct gtg atc agt ggg agc atc tgt ata ttg ttc ctg att ggc          3060
Leu Ser Val Ile Ser Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly
                1010            1015                1020

ctg atg tgt gga cgg atc acc aag cga gtg aca cga gag ctc aag          3105
Leu Met Cys Gly Arg Ile Thr Lys Arg Val Thr Arg Glu Leu LysA
                1025            1030                1035

gac agg tag
Asp Arg ***
        1038
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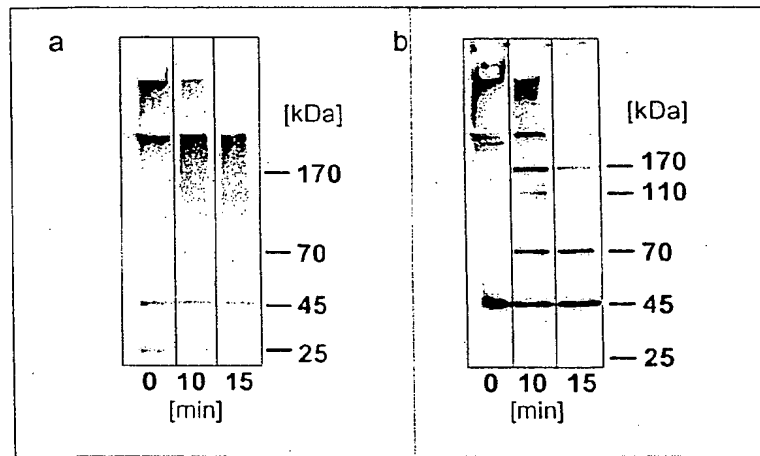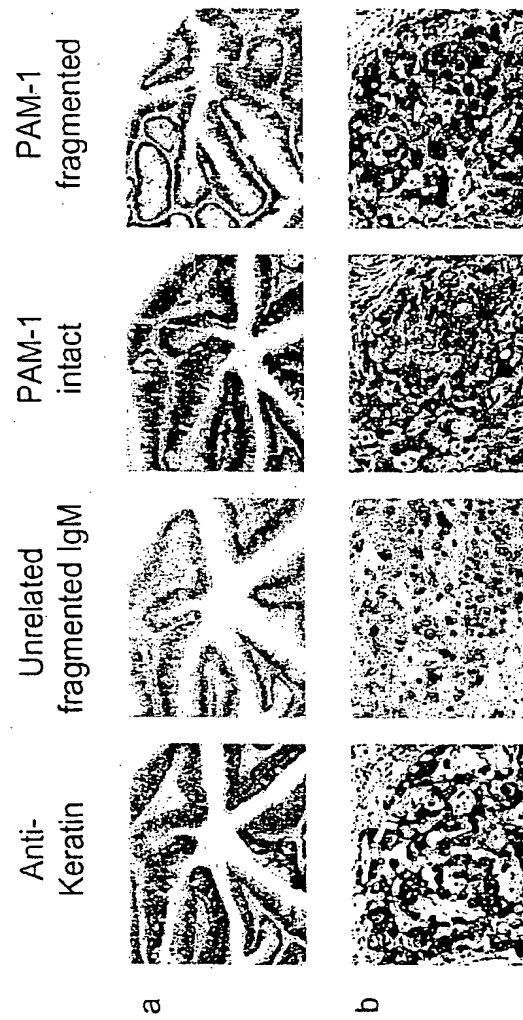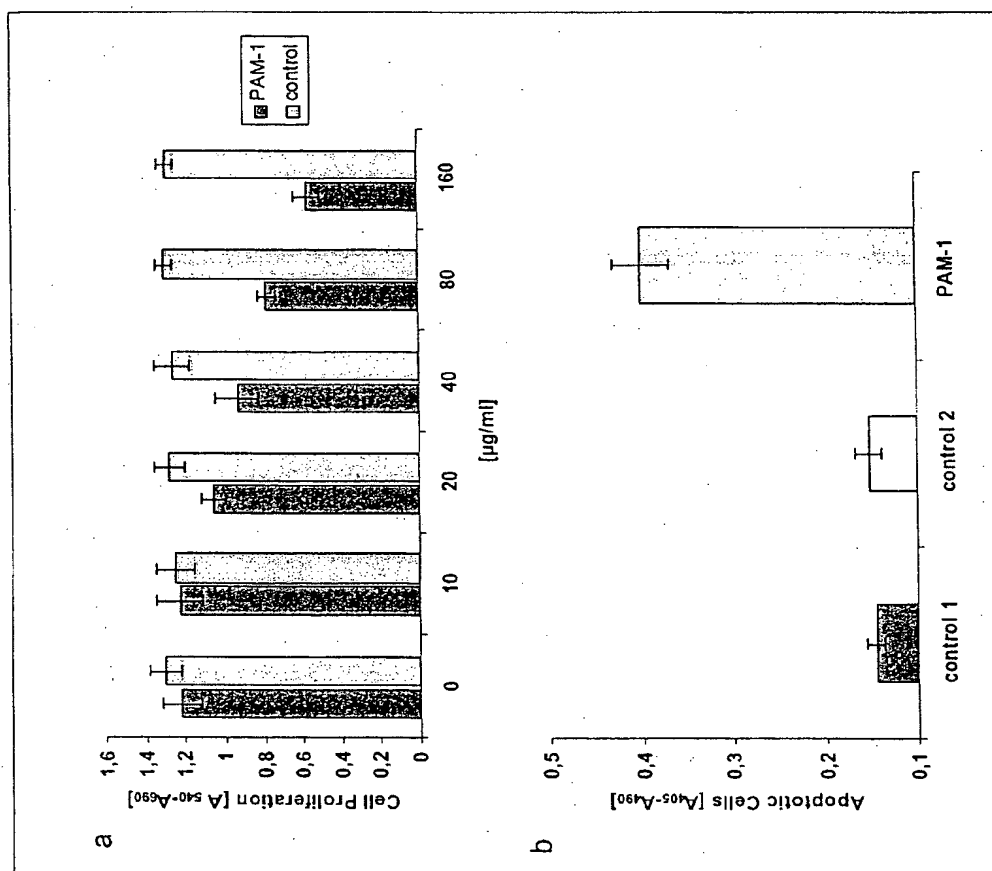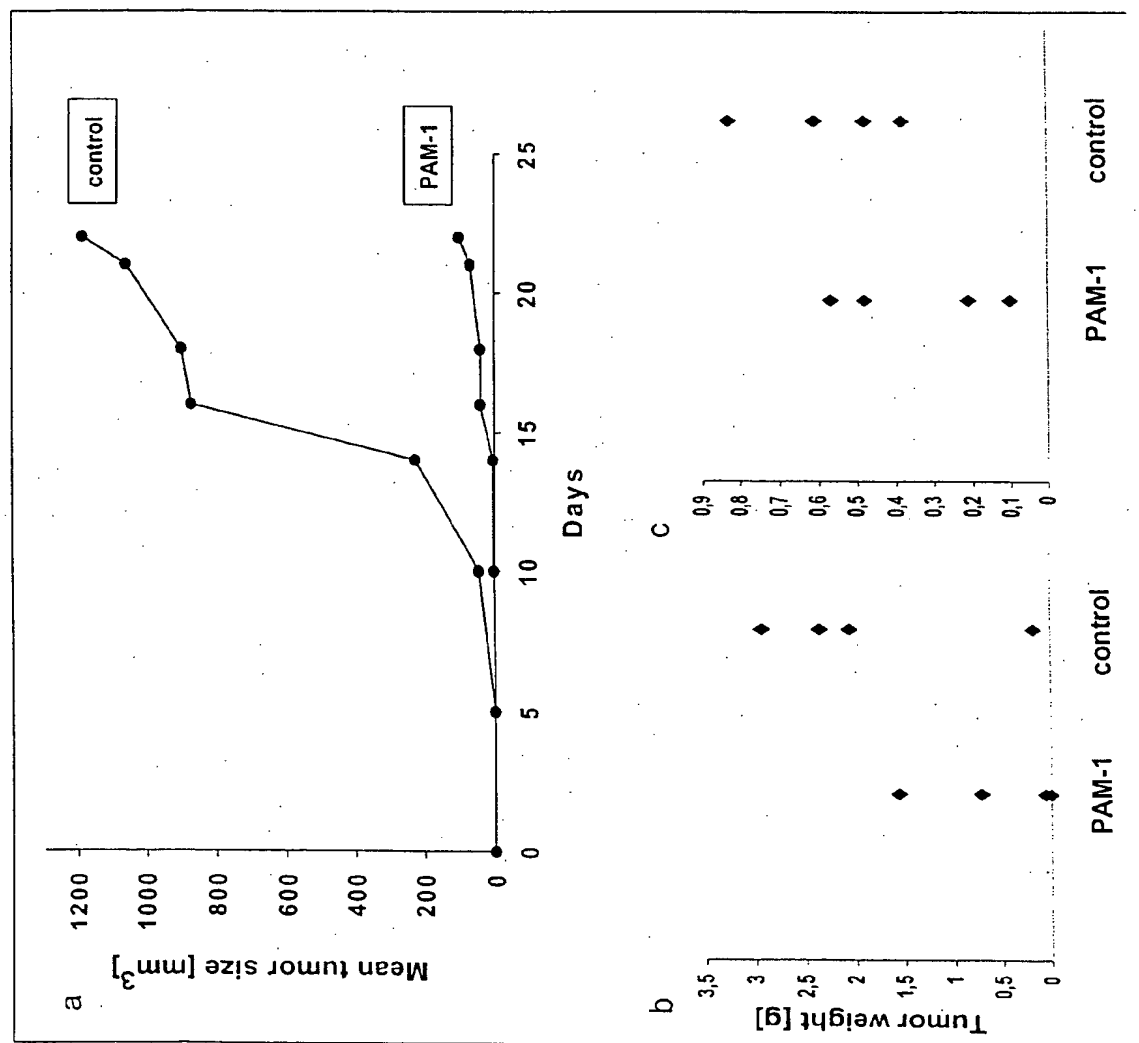
Fig. 10-5

Fig. 11

Fig. 12

Fig. 13

Fig. 14

Fig. 15

```
        1 23132 ----------  ----------  ----------  ----------  ----------  ----------  ----------  ----------  ----------  ----------
        1 CFR-1 MAACGRVRRM  FRLSRALHIL  LLFAAGGRNS  PARASHSGGQ  CPGANFVSFV  GQAGGGGPAG  QQLPLPQSS   QLQQQQQQQQ  QQQQ?QPPQP  PFPAGGPP-R
        1 MG160 MAACGRVRRM  FRLSAALHIL  LLFRAGAEKL  PGHGVHSGGQ  GPGANFVSFV  GQAGGGGPAG  QQLPLQSS    QLQQQQQQQQ  QQQQLQPPQP  PFPAGGPPAR

      101 23132 ----------  ----------  ----------  ----------  -DVREPENE   ISSDCNHLLM  NYKLNLTTDP  KEESVAREVC  KSTITEIKEC  ADEPVGKGYM
      101 CFR-1 RGGAGAGGGW  KLAEEESCRE  DVTRVCPKHT  WSNNLAVLEC  LQDVREPENE  ISSDCNHLLM  NYKLNLTTDP  KEESVAREVC  KST?TEIKEC  ADEPVGKGYM
      101 MG160 RGGAGAGGGW  KLAEEESCRE  DVTRVCPKHT  WSNNLAVLEC  LQDVREPENE  ISSDCNHLLM  NYKLNLTTDP  KEESVAREVC  KSTITEIKEC  ADEPVGKGYM

      201 23132 VSCLVDHRGN  ITEYQCHQYI  TKMTAIIFSD  YRLICGFMDD  CKNDINILKC  GSIRLGEKDA  HSQGEVVSCL  EKGLVKEAEE  REPKIQVSEL  CKKAILRVAE
      201 CFR-1 VSCLVDHRGN  ITEYQCHQYI  TKMTAIIFSD  YRLICGFMDD  CKNDINILKC  GSIRLGEKDA  HSQGEVVSCL  EKGLVKEAEE  REPKIQVSEL  CKKAILRVAE
      201 MG160 VSCLVDHRGN  ITEYQCHQYI  TKMTAIIFSD  YRLICGFMDD  CKNDINILKC  GSIRLGEKDA  HSQGEVVSCL  EKGLVKEAEE  REPKIQVSEL  CKKAILRVAE

      301 23132 LSSDDFHLDR  HLYFACRDDR  ERFCENTQAG  EGRVYKCLFN  HKFEESMSEK  CREALTTRQK  LEAQDYKVSY  SLAKSCKSDL  KKYRCNVENL  PRSREARLSY
      301 CFR-1 LSSDDFHLDR  HLYFACRDDR  ERFCENTQAG  EGRVYKCLFN  HKFEESMSEK  CREALTTRQK  LEAQDYKVSY  SLAKSCKSDL  KKYRCNVENL  PRSREARLSY
      301 MG160 LSSDDHHLDR  HLYFACRDDR  ERFCENTQAG  EGRVYKCLFN  HKFEESMSEK  CREALTTRQK  LEAQDYKVSY  SLAKSCKSDL  KKYRCNVENL  PRSREARLSY

      401 23132 LLMCLESAVH  KGRQVSSECQ  GEMLDYRRML  MEDFSLSPEI  ILSCRGEIEH  HCSGLHRKGR  TLHCLMKVVR  GEKGNLGMNC  QQALQTLIQE  TDPGADYRID
      401 CFR-1 LLMCLESAVH  KGRQVSSRCQ  GEMLDYRRML  MEDFSLSPEI  ILSCRGEEII  HCSGLHRKGR  TLHCLMKVVR  GEKGNLGMNC  QQALQTLIQE  TDPGADYRID
      401 MG160 LLMCLESAVH  KGRQVSSSCQ  GEMLDYRRML  MEDFSLSPEI  ILSCRGEEH   HCSGLHRKGR  TLHCLMKVVR  GEKGNLGMNC  QQALQTLIQE  TDPGADYRID

      501 23132 RALNEACESV  IQTACKHIRS  GDPMILSCLM  EHLYTEKMVE  DCEHRLLELQ  YFISRDWKLD  PVLYRKCQGD  ASRLCHTHGW  NETSEFMPQG  AVFSCLYRHA
      501 CFR-1 RALNEACESV  IQTACKHIRS  GDPMISSCLM  EHLYTEKMVE  DCEHRLLELQ  YFISRDWKLD  PVLYRKCQGD  ASRLCHTHGW  NETSEFMPQG  AVFSCLYRHA
      501 MG160 RALNEACESV  IQTACKHIRS  GDPMILSCLM  EHLYTEKMVE  DCEHRLLELQ  YFISRDWKLD  PVLYRKCQGD  ASRLCHTHGW  NETSEFMPQG  AVFSCLYRHA

      601 23132 YRTEEQGRRL  SRECRAEVQR  ILHQRAMDVK  LDPALQDKCL  IDLGKNGSEK  TETGQLECL   QDHLDLVVE   CRDIVGNLTE  LESEDIQIEA  LLMRACEPII
      601 CFR-1 YRTEEQGRRL  SRECRAEVQR  ILHQRAMDVK  LDPALQDKCL  IDLGKWCSEK  TETGQELECL  QDHLDLVVE   CRDIVGNLTE  LESEDIQIEA  LLMRACEPII
      601 MG160 YRTEEQGRRL  LDPALQDKCL  IDLGKWCSEK  SRECRAEVQR  ILHQRAMDVK  QDHLDLVVE   CRDIVGNLTE  LESEDIQIEA  LLMRACEPII

      701 23132 QNFCHDVADN  QIDSGDLMEC  LIQNKHQKDM  NEKCAIGVTH  FQLVQMKDFR  FSYKFKMACK  EDVLK.CPNI  KKKVDVVICL  STTVRNDTLQ  EAKEHRVSLK
      701 CFR-1 QTFCED-ADN  QIDSGDLMEC  LIQNKHQKDM  NEKCAIGVTH  FQLVQMKDFR  FSYKFKMACK  EDVLK.CPNI  KKKVDVVICL  STTVRNDTLQ  EAKEHRVSLK
      701 MG160 QNFCEDVADN  QIDSGDLMEC  LIQNKHQKDM  NEKCAIGVTH  FQLVQMKDFR  FSYKFKMACK  EDVLKLC2NI  KKKVDVVICL  STTVRNDTLQ  EAKEHRVSLK

      801 23132 CRRQLRVEEL  EMTEDIRLEP  DLYEACKSDI  KNFCSAVQYG  NAQIIECLKE  NKKQLSTRCH  QKVFKLQETE  MMDPELDYTL  MRVCKQMIKK  FCPEADSKTM
      801 CFR-1 CRRQLRVEEL  EMTEDIRLEP  DLYEACKSDI  KNFCSAVQYG  NAQIIECLKE  NKKQLSTRCH  QKVFKLQETE  MMDPELDYTL  MRVCKQMIKR  FCPEADSKTM
      801 MG160 CRRQLRVEEL  EMTEDIRLEP  DLYEACKSDI  KNFCSAVQYG  NAQIIECLKE  NKKQLSTRCH  QKVFKLQETE  MMDPELDYTL  MRVCKQMIKR  FCPEADSKTM

      901 23132 LQCLKQNKNS  ELMDPKCKQM  ITKRQITQNT  DYRLNPMLRK  ACKADIPKFC  HGILTKAKDD  SELEGQVISC  LKLRYADQRL  SSDCEDQIRI  IIQESALDYR
      901 CFR-1 LQCLKQNKNS  ELMDPKCKQM  ITKRQITQNT  DYRLNPMLRK  ACKADIPKFC  HGILTKAKDD  SELEGQVISC  LKLRYADQRL  SSDCEDQIRI  IIQESALDYR
      901 MG160 LQCLKQNKNS  ELMDPKCKQM  ITKRQITQNT  DYRLNPMLRK  ACKADIPKFC  HGILTKAKDD  SELEGQVISC  LKLRYADQRL  SSDCEDQIRI  IIQESALDYR

     1001 23132 LDPQLQLHCS  DEISSLCAEE  AAAQEQTGQV  EECLKVNLLK  IKTELCKKEV  LNMLKESKAD  -FVDPVLHTA  CALDIKHHCA  AITPGRGRQM  SCLMEALEDK
     1001 CFR-1 LDPQLQLHCS  DEISSLCAEE  AAAQEQTGGV  EECLKVNLLK  IKTELCKKEV  LNMLKESKAD  IFVDPVLHTA  CALDIKHHCA  ALTPGRGRQM  SCLMEALEDK
     1001 MG160 LDPQLQLHCS  DEISSLCAEE  AAAQEQTGQV  EECLKVNLLK  IKTELCKKEV  LNMLKESKAD  IFVDPVLHTA  CALDIKHHCA  AITPGRGRQM  SCLMEALEDK

     1101 23132 RVRLQPECKK  RLNDRIEMWS  YAAKVAPADG  FSDLAMQVMT  SPSKNYILSV  ISGSCILFL   IGLMCGRITK  RVTRELKDR*
     1101 CFR-1 RVRLQPECKK  RLNDRIEMWS  YAAKVAPADG  FSDLAMQVMT  SPSKNYILSV  ISGSCILFL   IGLMCGRITK  RVTRELKDR*
     1101 MG160 RVRLQPECKK  RLNDRIEMWS  YAAKVAPADG  FSDLAMQVMT  SPSKNYILSV  ISGSCILFL   IGLMCGRITK  RVTRELKDR*
```

Fig. 16

Human antibody PAM-1 (clone 103/51)

Heavy chain sequence

```
                                                CDR I
                                          _____
AGG TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT GGC    54
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly
            5                   10               15

ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GTT ATA   108
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile
    20                  25               30                  35

        CDR II
    _____
TCA TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG AAG GGC CGA TTC ACC   162
Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
            40              45                  50

ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA   216
Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
55                  60               65                  70
                                                        CDR III
                                                _____
GCT GAG GAC ACG GCT GTG TAT TAC TGT GCG AGG TCG ACT ACG AGG TCT TAT CCT   270
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Thr Thr Arg Ser Tyr Pro
            75                  80               85                  90

        CDR III
    _____
CTA TAC GGT ATG GAC GTT TGG GGC CAA GGG AAC CCT GTC ACC              312
Leu Tyr Gly Met Asp Val Trp Gly Gln Gly Asn Pro Val Thr
            95                  100
```

Fig. 17

Human antibody PAM-1 (clone 103/51)

Light chain sequence

```
GTG ACC TCC TAT GTG CTG ACT CAG CCA CCC TCG GTG TCA GTG GCC CCA GGA CAG    54
Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
            5               10                          15
                                            CDR I

ACG GCC AGT ATT ACC TGT GGG GGA AAT AAC ATT GGA AGT AAA AGT GTG CAC TGG   108
Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His Trp
        20              25                  30                      35

                                                        CDR II

TAC CAT CAG AAG CCA GGC CAG GCC CCT GTG CTG GTC GTC TAT GAT GAT AGC GAC   162
Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Asp Asp Ser Asp
                40              45                  50

CGG CCC TCA GGG ATC CCT GAG CGA TTC TCT GGC TCC AAC TCT GGG AAC ACG GCC   216
Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala
55                  60                  65                  70

ACC CTG ACC ATC ACC AGG GTC GAA GCC GGG GAT GAG GCC GAC TAT TAC TGT CAG   270
Thr Leu Thr Ile Thr Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln
        75                  80                  85                  90

        CDR III

GTG TGG GAT AGT AGT AGT GAT CTC AAT TGG GTG TTC GGC GGA AGG ACC CAA GCT   324
Val Trp Asp Ser Ser Ser Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala
                95              100                 105


GAC CGT CCT ACG TCA GCC CAA GGC TGC CCC TCC GGT CAC TCT GTT CCC CGC CCC   378
Asp Arg Pro Thr Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro
        110                 115                 120                 125

CCT CTG AAG AGC TTC AAG CTT   399
Pro Leu Lys Ser Phe Lys Leu
        130
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Fig. 18